CLAIMS

1.   A method for identifying mutations and/or polymorphisms that are major determinants of phenotype comprising examining the residual deviance (δ) for each selected group of mutations and/or polymorphisms of a gene under consideration.

2.   A method according to claim 1 wherein the residual deviance (δ) is determined for each subset of mutations and/or polymorphisms.

3.   A method according to claim 2 wherein the residual deviance (δ) of the partitioning of haplotypes {1...m} is based on each possible subset of mutations and/or polymorphisms.

4.   A method according to any preceding claim wherein the residual deviance (δ) equals $\delta = \delta(\Pi) = \sum_{i=1}^{m} (\chi_i - \bar{\chi}_{\pi(i)})^2$.

5.   The use of the method according to claims 1 to 4 for predicting super-maximal and/or sub-minimal haplotypes that are major determinants of a, corresponding, super-maximal phenotype and sub-minimal phenotype.

6.   The use of the methodology according to claims 1 to 4 for identifying single nucleotide polymorphisms SNPs that are of phenotypic significance.

7.   A detection method for detecting a haplotype effective to act as an indicator of at least one phenotype in an individual, which detection method comprises the steps of:

(a)   obtaining a test sample of genetic material from an individual to be tested, said material comprising, at least, a selected gene or a fragment thereof;

(b)   analysing the nucleotide sequence of said gene, or fragment thereof, to see if any single nucleotide polymorphisms (SNPs) exist at any one or more of the SNP sites within the gene; and

(c)   where said SNPs exist, identifying them in order to determine the haplotype of said individual and then subjecting said haplotype to the analysis according to claims 1 to 4 above.

8.   A phenotypically significant haplotype identified by the method of claims 1 to 4 for use in the diagnosis or treatment of a disease characterised by said phenotype.